

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Papathanassiu, Adonia E
Green, Shawn J.

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(ii) TITLE OF INVENTION: Compositions and Methods for
Inhibiting Cellular Proliferation

(iii) NUMBER OF SEQUENCES: 2

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Jones & Askew
(B) STREET: 191 Peachtree Street, 37th Floor
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: U.S.A.
20 (F) ZIP: 30303

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Greene, Jamie L.
(B) REGISTRATION NUMBER: 32,467
(C) REFERENCE/DOCKET NUMBER: 05213-0290

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: (404) 818-3700
(B) TELEFAX: (404) 818-3799

(2) INFORMATION FOR SEQ ID NO:1:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

25 (ix) FEATURE:
(A) NAME/KEY: Active-site
(B) LOCATION: 2..3
(D) OTHER INFORMATION: /note= "Site of partial phosphorylation"

30 (ix) FEATURE:
(A) NAME/KEY: Active-site
(B) LOCATION: 117..118
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

35 (ix) FEATURE:
(A) NAME/KEY: Active-site
(B) LOCATION: 167..168
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

40 (ix) FEATURE:
(A) NAME/KEY: Active-site
(B) LOCATION: 228..229
(D) OTHER INFORMATION: /note= "Potential site for N-linked glycosylation"

45 (ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 26..76
(D) OTHER INFORMATION: /label= Kunitz-1

(ix) FEATURE:

5 (A) NAME/KEY: Domain
 (B) LOCATION: 97..147
 (D) OTHER INFORMATION: /label= Kunitz-2

(ix) FEATURE:

10 (A) NAME/KEY: Domain
 (B) LOCATION: 189..239
 (D) OTHER INFORMATION: /label= Kunitz-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu
 1 5 10 15

Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp
 20 25 30

20 Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr
 35 40 45

Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn
 50 55 60

25 Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn
 65 70 75 80

30 Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe
 85 90 95

Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg
 100 105 110

35 Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly
 115 120 125

Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys
 130 135 140

40 Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly
 145 150 155 160

45 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys
 165 170 175

Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro
 180 185

Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn
195 200 205

5 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly
210 215 220

Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys
10 225 230 235 240

Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys
245 250 255

Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe
15 260 265 270

Val Lys Asn Met
275

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25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5	Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu
	1 5 10 15
	Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr
	20 25 30
10	Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu
	35 40 45
	Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys
	50 55 60
15	Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val
	65 70 75 80
20	Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser
	85 90 95
	Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg
	100 105 110
25	Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala
	115 120 125
	Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu
	130 135 140
30	Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr
	145 150 155 160
35	Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe
	165 170 175
	Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys
	180 185 190
40	Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile
	195 200 205
	Arg Lys Lys Gln Phe
	210
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